



SEQUENCE LISTING

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Weiner, David P.
Chaplin, Jennifer A.

<120> METHODS FOR PRODUCING ENANTIOMERICALLY PURE
ALPHA-SUBSTITUTED CARBOXYLIC ACIDS

<130> DIVER1440-2

<140> US 09/751,299

<141> 2000-12-28

<150> 60/254,414

<151> 2000-12-07

<150> 60/173,609

<151> 1999-12-29

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1041

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Obtained from an
environmental sample

<220>

<221> CDS

<222> (1)..(1041)

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atg	tcg	gag	ccc	atg	acg	aag	tat	cgc	ggc	gcg	gcg	gtg	cag	gcc	gcg	48
Met	Ser	Glu	Pro	Met	Thr	Lys	Tyr	Arg	Gly	Ala	Ala	Val	Gln	Ala	Ala	
1				5				10						15		

ccg	gtg	ttc	ctc	gat	ctc	gac	cgc	aca	gtc	gag	aaa	gcg	atc	ggc	ctg	96
Pro	Val	Phe	Leu	Asp	Leu	Asp	Arg	Thr	Val	Glu	Lys	Ala	Ile	Gly	Leu	
			20					25						30		

atc	gag	cag	gcg	gcc	aag	cag	gac	gtg	cgc	ctg	atc	gca	ttc	cca	gag	144
Ile	Glu	Gln	Ala	Ala	Lys	Gln	Asp	Val	Arg	Leu	Ile	Ala	Phe	Pro	Glu	
			35					40						45		

act	tgg	att	ccc	ggc	tat	ccc	ttt	tgg	ata	tgg	ctg	ggc	gcg	ccg	gct	192
Thr	Trp	Ile	Pro	Gly	Tyr	Pro	Phe	Trp	Ile	Trp	Leu	Gly	Ala	Pro	Ala	
	50					55					60					

tgg	ggc	atg	cgc	ttc	gtc	cag	cgc	tat	ttc	gag	aat	tcg	ctc	gtg	cgc	240
Trp	Gly	Met	Arg	Phe	Val	Gln	Arg	Tyr	Phe	Glu	Asn	Ser	Leu	Val	Arg	
	65					70				75					80	

ggc	agc	aag	cag	tgg	cag	gcc	ctg	gcg	gat	gcg	gcc	cgc	cgc	cac	ggc	288
Gly	Ser	Lys	Gln	Trp	Gln	Ala	Leu	Ala	Asp	Ala	Ala	Arg	Arg	His	Gly	
				85					90						95	

atg cat gtc gtg gcc ggc tat agc gag cgc gcg ggc ggc agc ctc tat	336
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr	
100 105 110	
atg ggc cag gcg atc ttc ggc ccc gat ggc gat ctg atc gcc gcg cgc	384
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg	
115 120 125	
cgc aag ctc aag cct acc cat gcg gag cgc acc gtg ttc ggc gag gga	432
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly	
130 135 140	
gac ggc agc cat ctc gcg gtg cac gat acc gcc atc ggg cgc ctc ggc	480
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly	
145 150 155 160	
gcg ctc tgt tgc tgg gag cac atc cag cca ttg tcg aaa tac gcc atg	528
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met	
165 170 175	
tac gcc gcc gac gaa cag gtc cac gtc gcg tcg tgg ccg agc ttc agc	576
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser	
180 185 190	
ctc tat cgc ggc atg gcc tat gcg ctc gga ccg gag gtc aat acc gcc	624
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala	
195 200 205	
gca agc cag atc tac gcg gtc gag ggc ggc tgc tac gtg ctg gcg tcg	672
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser	
210 215 220	
tgc gcg acc gtt tcg ccg gag atg atc aag gta ttg gtg gat acg ccc	720
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro	
225 230 235 240	
gac aag gag atg ttc ctc aag gcc ggc ggc ggt ttt gcc atg att ttc	768
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Gly Phe Ala Met Ile Phe	
245 250 255	
ggg ccc gac ggc cgc gcc ctg gcc gag ccg ctc ccg gag acc gaa gag	816
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu	
260 265 270	
gga ctg ctg gtc gcc gat atc gac ctc ggc atg atc gcg ttg gcc aag	864
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys	
275 280 285	
gcg gcg gcc gat ccg gcg ggc cac tat tca cgg ccc gac gta acg cgg	912
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg	
290 295 300	
ctg ctg ctg gat cga cgt ccg gcc caa cgc gtc gtc acg ctt gat gcc	960
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala	
305 310 315 320	
gca ttc gaa ccg caa aac gag gac aag ggc gac gcg ccc gcg ctg cgc	1008
Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg	
325 330 335	

gtg gtg gcg gaa agc gcc gcc gcc gcg cag tag
 Val Val Ala Glu Ser Ala Ala Ala Ala Gln
 340 345

1041

<210> 2
 <211> 346
 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: Obtained from an
 environmental sample

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 Met Ser Glu Pro Met Thr Lys Tyr Arg Gly Ala Ala Val Gln Ala Ala
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 Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu
 20 25 30
 Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala
 50 55 60
 Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg
 65 70 75 80
 Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly
 85 90 95
 Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr
 100 105 110
 Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg
 115 120 125
 Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly
 130 135 140
 Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly
 145 150 155 160
 Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met
 165 170 175
 Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser
 180 185 190
 Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala
 195 200 205
 Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser
 210 215 220
 Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro
 225 230 235 240
 Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Gly Phe Ala Met Ile Phe
 245 250 255
 Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu
 260 265 270
 Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys
 275 280 285
 Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg
 290 295 300
 Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala
 305 310 315 320
 Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg
 325 330 335
 Val Val Ala Glu Ser Ala Ala Ala Ala Gln
 340 345

<210> 3

<211> 1014
 <212> DNA
 <213> Unknown Organism

<220>

<223> Description of Unknown Organism: Obtained from an
 environmental sample

<220>

<221> CDS

<222> (1)..(1014)

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Met	Lys	Glu	Ala	Ile	Lys	Val	Ala	Cys	Val	Gln	Ala	Ala	Pro	Ile	Tyr	
1				5				10						15		
atg	gat	ttg	gag	gcg	acg	gtg	gac	aaa	acc	att	gag	ttg	atg	gaa	gaa	96
Met	Asp	Leu	Glu	Ala	Thr	Val	Asp	Lys	Thr	Ile	Glu	Leu	Met	Glu	Glu	
		20						25					30			
gca	gca	cgt	aat	aat	gct	cgt	ctg	atc	gcc	ttt	ccg	gaa	act	tgg	att	144
Ala	Ala	Arg	Asn	Asn	Ala	Arg	Leu	Ile	Ala	Phe	Pro	Glu	Thr	Trp	Ile	
		35					40					45				
cca	ggc	tac	cca	tgg	ttt	ctt	tgg	ctt	gac	tca	cca	gca	tgg	gca	atg	192
Pro	Gly	Tyr	Pro	Trp	Phe	Leu	Trp	Leu	Asp	Ser	Pro	Ala	Trp	Ala	Met	
	50					55					60					
caa	ttt	gta	cgc	caa	tac	cat	gag	aac	tca	ttg	gag	ttg	gat	ggc	cct	240
Gln	Phe	Val	Arg	Gln	Tyr	His	Glu	Asn	Ser	Leu	Glu	Leu	Asp	Gly	Pro	
65				70				75						80		
caa	gct	aag	cgc	att	tca	gat	gca	gcc	aag	cgg	ttg	gga	atc	atg	gtc	288
Gln	Ala	Lys	Arg	Ile	Ser	Asp	Ala	Ala	Lys	Arg	Leu	Gly	Ile	Met	Val	
				85				90						95		
acc	ctg	ggg	atg	agt	gaa	cgg	gtc	ggg	ggc	acc	ctt	tac	atc	agt	cag	336
Thr	Leu	Gly	Met	Ser	Glu	Arg	Val	Gly	Gly	Thr	Leu	Tyr	Ile	Ser	Gln	
		100						105					110			
tgg	ttc	ata	ggc	gat	aat	ggg	gac	acc	att	ggg	gcc	cgg	cga	aag	ttg	384
Trp	Phe	Ile	Gly	Asp	Asn	Gly	Asp	Thr	Ile	Gly	Ala	Arg	Arg	Lys	Leu	
		115					120					125				
aaa	cct	act	ttt	gtt	gaa	cgt	act	ttg	ttc	ggc	gaa	ggg	gat	ggg	tca	432
Lys	Pro	Thr	Phe	Val	Glu	Arg	Thr	Leu	Phe	Gly	Glu	Gly	Asp	Gly	Ser	
	130					135					140					
tcg	cta	gcg	gtt	ttc	gag	acg	tct	gtt	gga	agg	ctg	ggg	ggc	tta	tgc	480
Ser	Leu	Ala	Val	Phe	Glu	Thr	Ser	Val	Gly	Arg	Leu	Gly	Gly	Leu	Cys	
145					150				155						160	
tgt	tgg	gag	cac	ctt	caa	ccg	cta	aca	aaa	tac	gct	ttg	tat	gca	caa	528
Cys	Trp	Glu	His	Leu	Gln	Pro	Leu	Thr	Lys	Tyr	Ala	Leu	Tyr	Ala	Gln	
				165				170						175		
aat	gaa	gag	att	cat	tgt	gcg	gct	tgg	ccg	agc	ttt	agc	ctt	tat	cct	576
Asn	Glu	Glu	Ile	His	Cys	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	Tyr	Pro	
			180					185						190		

aat gcg gcg aaa gcc ctg ggg cct gat gtc aat gta gcg gcc tct cga	624
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg	
195 200 205	
atc tat gcc gtt gaa ggg caa tgc ttc gta cta gcg tcg tgt gcg ctc	672
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu	
210 215 220	
gtt tca caa tcc atg atc gat atg ctt tgt aca gat gac gaa aag cat	720
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His	
225 230 235 240	
gcg ttg ctt ctg gct ggt ggt gga cac tca cgt atc ata ggg cct gat	768
Ala Leu Leu Leu Ala Gly Gly Gly His Ser Arg Ile Ile Gly Pro Asp	
245 250 255	
ggg ggt gac ttg gtc gcg cct ctt gcc gaa aat gaa gag ggt att ctc	816
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu	
260 265 270	
tac gca aac ctt gat cct gga gta cgc atc ctt gct aaa atg gcg gca	864
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala	
275 280 285	
gac cct gct ggt cat tat tcc cgt ccc gac att act cgc ttg cta ata	912
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile	
290 295 300	
gat cgc agc cct aaa tta ccg gta gtt gaa att gaa ggt gat ctt cgt	960
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg	
305 310 315 320	
cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa	1008
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu	
325 330 335	
att tga	1014
Ile	

<210> 4

<211> 337

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: Obtained from an environmental sample

<400> 4

Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr	
1 5 10 15	
Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu	
20 25 30	
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile	
35 40 45	
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met	
50 55 60	
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro	
65 70 75 80	
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val	
85 90 95	
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln	

[illegible]